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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/892,287

DATE: 03/27/2003

TIME: 12:39:41

Input Set : A:\pf03342div\_substitute sequence listing.txt

Output Set: N:\CRF4\03272003\I892287.raw

5-

1 <110> APPLICANT: Hillman, Jennifer L.; Lal, Preeti G.;

2 Corley, Neil C.; Shah, Purvi

4 <120> TITLE OF INVENTION: ANTIBODIES TO A HUMAN PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE

5 PHOSPHATASE (As amended)

7 <130> FILE REFERENCE: PF-0334-2 DIV

9 <140> CURRENT APPLICATION NUMBER: 09/892,287

10 <141> CURRENT FILING DATE: 2001-06-26

12 <150> PRIOR APPLICATION NUMBER: US 09/258,643

13 <151> PRIOR FILING DATE: 1999-02-26

15 <150> PRIOR APPLICATION NUMBER: US 08/884,681

16 <151> PRIOR FILING DATE: 1997-06-27

18 <160> NUMBER OF SEQ ID NOS: 5

19 <170> SOFTWARE: PERL Program

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 372

23 <212> TYPE: PRT

24 <213> ORGANISM: Homo sapiens

26 <220> FEATURE:

27 <221> NAME/KEY: misc\_feature

28 <223> OTHER INFORMATION: Incyte ID No: 638789CD1

30 <400> SEQUENCE: 1

31 Met Asp Val Leu Ser Pro Leu Ser Phe Ile Lys Val Ser His Val

32 1 5 10 15

33 Arg Met Gln Gly Ile Leu Leu Leu Val Phe Ala Lys Tyr Gln His

34 20 25 30

35 Leu Pro Tyr Ile Gln Ile Leu Ser Thr Lys Ser Thr Pro Thr Gly

36 35 40 45

37 Leu Phe Gly Tyr Trp Gly Asn Lys Gly Gly Val Asn Ile Cys Leu

38 50 55 60

39 Lys Leu Tyr Gly Tyr Tyr Val Ser Ile Ile Asn Cys His Leu Pro

40 65 70 75

41 Pro His Ile Ser Asn Asn Tyr Gln Arg Leu Glu His Phe Asp Arg

42 80 85 90

43 Ile Leu Glu Met Gln Asn Cys Glu Gly Arg Asp Ile Pro Asn Ile

44 95 100 105

45 Leu Asp His Asp Leu Ile Ile Trp Phe Gly Asp Met Asn Phe Arg

46 110 115 120

47 Ile Glu Asp Phe Gly Leu His Phe Val Arg Glu Ser Ile Lys Asn

48 125 130 135

49 Arg Cys Tyr Gly Gly Leu Trp Glu Lys Asp Gln Leu Ser Ile Ala

50 140 145 150

51 Lys Lys His Asp Pro Leu Leu Arg Glu Phe Gln Glu Gly Arg Leu

52 155 160 165

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53 Leu Phe Pro Pro Thr Tyr Lys Phe Asp Arg Asn Ser Asn Asp Tyr
54                               170                     175                     180
55 Asp Thr Ser Glu Lys Lys Arg Lys Pro Ala Trp Thr Asp Arg Ile
56                               185                     190                     195
57 Leu Trp Arg Leu Lys Arg Gln Pro Cys Ala Gly Pro Asp Thr Pro
58                               200                     205                     210
59 Ile Pro Pro Ala Ser His Phe Ser Leu Ser Leu Arg Gly Tyr Ser
60                               215                     220                     225
61 Ser His Met Thr Tyr Gly Ile Ser Asp His Lys Pro Val Ser Gly
62                               230                     235                     240
63 Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser Ala Pro Leu Ile
64                               245                     250                     255
65 Val Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn Asp Met Met
66                               260                     265                     270
67 Val Ser Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro Trp Asp
68                               275                     280                     285
69 Trp Ile Gly Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp Tyr
70                               290                     295                     300
71 Val Ser Tyr Ala Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp
72                               305                     310                     315
73 Asn Leu Asn Gln Val Tyr Ile Asp Ile Ser Asn Ile Pro Thr Thr
74                               320                     325                     330
75 Glu Asp Glu Phe Leu Leu Cys Tyr Tyr Ser Asn Ser Leu Arg Ser
76                               335                     340                     345
77 Val Val Gly Ile Ser Arg Pro Phe Gln Ile Pro Pro Gly Ser Leu
78                               350                     355                     360
79 Arg Glu Asp Pro Leu Gly Glu Ala Gln Pro Gln Ile
80                               365                     370

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82 &lt;210&gt; SEQ ID NO: 2

83 &lt;211&gt; LENGTH: 2573

84 &lt;212&gt; TYPE: DNA

85 &lt;213&gt; ORGANISM: Homo sapiens

87 &lt;220&gt; FEATURE:

88 &lt;221&gt; NAME/KEY: misc feature

89 &lt;223&gt; OTHER INFORMATION: Incyte ID No: 638789CB1

91 &lt;400&gt; SEQUENCE: 2

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92 gaaggctcag catacacgtc gtgacttgga acgtggcttc ggcagcgccc ctcgagctct 60
93 cagtgacctg cttcagctga acaaccggaa cctcaatctt gacatatatg ttattgggtt 120
94 gcaggaattg aactctggga tcataagcct cctttccgat gctgccttta atgactcgtg 180
95 gagcagtttc ctcatggatg tgctttcccc tctgagcttc atcaaggctt cccatgtccg 240
96 tatgcagggg atcctcttac tggcttttgc caagtatcag catttgccct atatccagat 300
97 tctgtctact aaatccaccc ccactggcct gtttgggtac tgggggaaca aaggtggagt 360
98 caacatctgc ctgaagcttt atggctacta tgtcagcatc atcaactgcc acctgcctcc 420
99 ccacatttcc aacaattacc agcggctgga gcactttgac cggatcctgg agatgcagaa 480
100 ttgtgagggg cgagacatcc caaacatcct ggaccacgac ctcattatct ggtttggaga 540
101 catgaacttt cggatcgagg actttgggtt gcactttgtt cggaatcca ttaaaaatcg 600
102 gtgctacggt ggctgtggg agaaggacca gctcagcatt gccaagaaac atgacccgct 660
103 gctccgggag ttccaggagg gccgcctact cttccgccc acctacaagt ttgataggaa 720
104 ctccaacgac tatgacacca gtgagaaaaa acgcaagcct gcatggaccg atcgcatcct 780

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```

105 gtggaggctg aagcggcagc cctgtgctgg ccccgacact cccataccgc cggcgtcaca 840
106 cttctccttg tctctgaggg gctacagcag ccacatgacg tacggcatca gcgaccacaa 900
107 gcctgtctcc ggcacgttcg acttgagct gaagccattg gtgtctgctc cgctgatcgt 960
108 cctgatgccc gaggacctgt ggaccgtgga aaatgacatg atggtcagct actcttcaac 1020
109 ctcggaactc cccagcagcc cgtgggactg gattggactg tacaagggtg ggctgcggga 1080
110 cgttaatgac tacgtgtcct atgcctgggt cggggacagc aaggtctcct gcagcgacaa 1140
111 cctgaaccag gtttacatcg acatcagcaa tatccctacc actgaagatg agtttctcct 1200
112 ctgttactac agcaacagtc tgcgttctgt ggtggggata agcagaccct tccagatccc 1260
113 gcctggctcc ttgagggagg acccactggg tgaagcacag ccacagatct gagccaggat 1320
114 gggagtgaat cccaggcggg ggccagagct ggcagccagc tctgccttcc cactgcgggg 1380
115 agtgctgggg gccagcctg gccccctgaa gagacagcca agtgctgctc acatactcct 1440
116 cccagagtga gctctaacca ggctcatttg ctctctccac tactcatctc tggaattagc 1500
117 cgcttaaata cagggtttttg ttgctgagat gtgagtgaag ccagctagtg tgtcaacagt 1560
118 gaagacctgg ggacagttct gcgtctcatt tctggattcc taccctctct tctagtcttg 1620
119 cccaagtagt cctgccaggc acatgcccc a tttggcacag gcctgcattc ttgtcgtgcc 1680
120 gtccctggggc tcaggctgtc tgggagggga gatgctcaca tttgtacagg ctacatagac 1740
121 tggtgcaagc agtgctggat tccaggagtc ttggcatctc atagcttgct cccgtgagga 1800
122 gtgagcagag ggtctgggat ttctgcttcc agcaaaagca gtctgactca gtgggcagaa 1860
123 tggagggggc cctctagcca ggctcttacg ccattggtat gagcagggtg atgaggggtc 1920
124 ttgggccagc acaaccttcc tccctactca cggcatggag tctgactgca tggaagtcc 1980
125 agatcctgac agagagaact gggaaggatc cagggttcgct tccgttggtg gcttgagtcc 2040
126 catgcctcca cctgccatc tgaggaaggg gtgacaagtg gtcaaggagc tgtggccaca 2100
127 gacttttcca ggggtgtcct tggcaggtag ggtgcgtctg tgccaccctt gtcaggagtc 2160
128 attgacgagc ggccccctc ggacccccg ggacctcaga gtgggggcag gcagaaggga 2220
129 gaaccagctc aagacatttt ggaggatctg gccctggggt tcttcagaga acaccctcta 2280
130 ggggcttttg ggacatggcc tgtccccaca tccagcactt gcctccgcca tggctactcg 2340
131 gcagcccttt tcccaggaga agacacctc tggagcctgc tcagtgttg tccctgccatc 2400
132 ctgtgtcctg ggactgaggg ttactccagt tgctctgtgt tgcatactct cccccgcaag 2460
133 cctgtgtatg aagaattgtc ccctggcttc cagcaggcca tggctggctg ttttgtgact 2520
134 gttacattgt gcaggggtaa ttattagcgt ggcttttaca cttaaaaaaa aaa 2573

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136 &lt;210&gt; SEQ ID NO: 3

137 &lt;211&gt; LENGTH: 397

138 &lt;212&gt; TYPE: PRT

139 &lt;213&gt; ORGANISM: Homo sapiens

141 &lt;220&gt; FEATURE:

142 &lt;221&gt; NAME/KEY: misc\_feature

143 &lt;223&gt; OTHER INFORMATION: GenBank ID No: g1399105

145 &lt;400&gt; SEQUENCE: 3

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146 Ala Arg Gly Leu His Phe Val Lys Phe Ala Ile Asp Ser Asp Gln
147   1                      5                      10                      15
148 Leu His Gln Leu Trp Glu Lys Asp Gln Leu Asn Met Ala Lys Asn
149                      20                      25                      30
150 Thr Trp Pro Ile Leu Lys Gly Phe Gln Glu Gly Pro Leu Asn Phe
151                      35                      40                      45
152 Ala Pro Thr Phe Lys Phe Asp Val Gly Thr Asn Lys Tyr Asp Thr
153                      50                      55                      60
154 Ser Ala Lys Lys Arg Lys Pro Ala Trp Thr Asp Arg Ile Leu Trp
155                      65                      70                      75
156 Lys Val Lys Ala Pro Gly Gly Gly Pro Ser Pro Ser Gly Arg Lys

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157		80		85		90
158	Ser His Arg Leu Gln Val Thr Gln His Ser Tyr Arg Ser His Met					
159		95		100		105
160	Glu Tyr Thr Val Ser Asp His Lys Pro Val Ala Ala Gln Phe Leu					
161		110		115		120
162	Leu Gln Phe Ala Phe Arg Asp Asp Met Pro Leu Val Arg Leu Glu					
163		125		130		135
164	Val Ala Asp Glu Trp Val Arg Pro Glu Gln Ala Val Val Arg Tyr					
165		140		145		150
166	Arg Met Glu Thr Val Phe Ala Arg Ser Ser Trp Asp Trp Ile Gly					
167		155		160		165
168	Leu Tyr Arg Val Gly Phe Arg His Cys Lys Asp Tyr Val Ala Tyr					
169		170		175		180
170	Val Trp Ala Lys His Glu Asp Val Asp Gly Asn Thr Tyr Gln Val					
171		185		190		195
172	Thr Phe Ser Glu Glu Ser Leu Pro Lys Gly His Gly Asp Phe Ile					
173		200		205		210
174	Leu Gly Tyr Tyr Ser His Asn His Ser Ile Leu Ile Gly Ile Thr					
175		215		220		225
176	Glu Pro Phe Gln Ile Ser Leu Pro Ser Ser Glu Leu Ala Ser Ser					
177		230		235		240
178	Ser Thr Asp Ser Ser Gly Thr Ser Ser Glu Gly Glu Asp Asp Ser					
179		245		250		255
180	Thr Leu Glu Leu Leu Ala Pro Lys Ser Arg Ser Pro Ser Pro Gly					
181		260		265		270
182	Lys Ser Lys Arg His Arg Ser Arg Ser Pro Gly Leu Ala Arg Phe					
183		275		280		285
184	Pro Gly Leu Ala Leu Arg Pro Ser Ser Arg Glu Arg Arg Gly Ala					
185		290		295		300
186	Ser Arg Ser Pro Ser Pro Gln Ser Arg Arg Leu Ser Arg Val Ala					
187		305		310		315
188	Pro Asp Arg Ser Ser Asn Gly Ser Ser Arg Gly Ser Ser Glu Glu					
189		320		325		330
190	Gly Pro Ser Gly Leu Pro Gly Pro Trp Ala Phe Pro Pro Ala Val					
191		335		340		345
192	Pro Arg Ser Leu Gly Leu Leu Pro Ala Leu Arg Leu Glu Thr Val					
193		350		355		360
194	Asp Pro Gly Gly Gly Gly Ser Trp Gly Pro Asp Arg Glu Ala Leu					
195		365		370		375
196	Ala Pro Asn Ser Leu Ser Pro Ser Pro Gln Gly His Arg Gly Leu					
197		380		385		390
198	Glu Glu Gly Gly Leu Gly Pro					
199		395				
201	<210> SEQ ID NO: 4					
202	<211> LENGTH: 942					
203	<212> TYPE: PRT					
204	<213> ORGANISM: Homo sapiens					
206	<220> FEATURE:					
207	<221> NAME/KEY: misc_feature					

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208 &lt;223&gt; OTHER INFORMATION: GenBank ID No: g1019103

210 &lt;400&gt; SEQUENCE: 4

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211 Val Thr Val Pro Glu Pro Gly Ala Ala Glu Ser Arg Ala Pro Cys
212 1 5 10 15
213 Gly Asp Ser Ser Gly Gly Cys Val Arg Ser Ala Gly Ala Ser Met
214 20 25 30
215 Asp Gln Ser Val Ala Ile Gln Glu Thr Leu Ala Glu Gly Glu Tyr
216 35 40 45
217 Cys Val Ile Ala Val Gln Gly Val Leu Cys Glu Gly Asp Ser Arg
218 50 55 60
219 Gln Ser Arg Leu Leu Gly Leu Val Arg Tyr Arg Leu Glu His Gly
220 65 70 75
221 Gly Gln Glu His Ala Leu Phe Leu Tyr Thr His Arg Arg Met Ala
222 80 85 90
223 Ile Thr Gly Asp Asp Val Ser Leu Asp Gln Ile Val Pro Val Ser
224 95 100 105
225 Arg Asp Phe Thr Leu Glu Glu Val Ser Pro Asp Gly Glu Leu Tyr
226 110 115 120
227 Ile Leu Gly Ser Asp Val Thr Val Gln Leu Asp Thr Ala Glu Leu
228 125 130 135
229 Ser Leu Val Phe Gln Leu Pro Phe Gly Ser Gln Thr Arg Met Phe
230 140 145 150
231 Leu His Glu Val Ala Arg Ala Cys Pro Gly Phe Asp Ser Ala Thr
232 155 160 165
233 Arg Asp Pro Glu Phe Leu Trp Leu Ser Arg Tyr Arg Cys Ala Glu
234 170 175 180
235 Leu Glu Leu Glu Met Pro Thr Pro Arg Gly Cys Asn Ser Ala Leu
236 185 190 195
237 Val Thr Trp Pro Gly Tyr Ala Thr Ile Gly Gly Gly Gly Ser Asn
238 200 205 210
239 Phe Asp Gly Leu Arg Pro Asn Gly Lys Gly Val Pro Met Asp Gln
240 215 220 225
241 Ser Ser Arg Gly Gln Asp Lys Pro Glu Ser Leu Gln Pro Arg Gln
242 230 235 240
243 Asn Lys Ser Lys Ser Glu Ile Thr Asp Met Val Arg Ser Ser Thr
244 245 250 255
245 Ile Thr Val Ser Asp Lys Ala His Ile Leu Ser Met Gln Lys Phe
246 260 265 270
247 Gly Leu Arg Asp Thr Ile Val Lys Ser His Leu Leu Gln Lys Glu
248 275 280 285
249 Glu Asp Tyr Thr Tyr Ile Gln Asn Phe Arg Phe Phe Ala Gly Thr
250 290 295 300
251 Tyr Asn Val Asn Gly Gln Ser Pro Lys Glu Cys Leu Arg Leu Trp
252 305 310 315
253 Leu Ser Asn Gly Ile Gln Ala Pro Asp Val Tyr Cys Val Gly Phe
254 320 325 330
255 Gln Glu Leu Asp Leu Ser Lys Glu Ala Phe Phe Phe His Asp Thr
256 335 340 345
257 Pro Lys Glu Glu Glu Trp Phe Lys Ala Val Ser Glu Gly Leu His

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**VERIFICATION SUMMARY**

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Input Set : A:\pf03342div\_\_substitute sequence listing.txt

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